

## RAW SEQUENCE LISTING

DATE: 01/14/2002

PATENT APPLICATION: US/09/645,337

TIME: 15:18:06

Input Set : A:\104701.01 Sequence Listing.txt

Output Set: N:\CRF3\01112002\I645337.raw

ENTERED

5 <110> APPLICANT: Wu Dr., Keqiang  
7 Miki Dr., Brian L  
9 Tian Dr., Lining  
11 Brown Dr., Dan  
14 <120> TITLE OF INVENTION: Repressing Gene Expression in Plants  
17 <130> FILE REFERENCE: 104107.01  
20 <140> CURRENT APPLICATION NUMBER: 09/645,337  
22 <141> CURRENT FILING DATE: 2000-08-25  
26 <150> PRIOR APPLICATION NUMBER: US 09/383,971  
28 <151> PRIOR FILING DATE: 1999-08-27  
32 <160> NUMBER OF SEQ ID NOS: 11  
36 <170> SOFTWARE: PatentIn Ver. 2.0  
40 <210> SEQ ID NO: 1  
42 <211> LENGTH: 1807  
44 <212> TYPE: DNA  
46 <213> ORGANISM: Arabidopsis thaliana  
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56 tgatcctacg aaaaagaggt aatggatact ggcggaatt cgctggcgct cggacctgat 180  
58 ggtgtgaaga ggaaagtgtg ttatttctat gacctgagg tcggcaatta ctactatggc 240  
60 caaggctacc ccatgaagcc ccacgcacac cgcacgccc atgcccctct cgctcactac 300  
62 ggtctctctc agcatatgca ggttctcaag ccttccctg ccgcggaacg tgatctctgc 360  
64 cgcttccacg ccgacgacta tgtctctttt ctccgcagca ttaccctga aaccacgcaa 420  
66 gatcagattc gccaaactaa gcgcttcaat gttggtgaag actgtcccgt ctttgacggc 480  
68 ctttattcct ttgcccagac ctatgctgga ggatctgttg gtggtctgt caagctaac 540  
70 caccgctctc gcgatattgc catcaactgg gctggtggtc tccatcacgc taagaagtgc 600  
72 gaggcctctg gcttctgtta cgtcaatgat atcgtcttag ctactctaga gctccttaag 660  
74 cagcatgagc gtgttcttta tgcgatatt gatattccac acggggatgg agtggaggag 720  
76 gcattttatg ctactgacag ggttatgact gtctcgtttc ataaatttgg tgattacttt 780  
78 ccgggtacag gtcacattca ggatataggt tatggtagcg gaaagtacta ttctctcaat 840  
80 gtaccactgg atgatggaat cgatgatgag agctatcacc tgttattcaa gcccatcatg 900  
82 gggaaagtta tggaaatttt ccgaccaggg gctgtggtat tgcaatgtgg tgcgtactcc 960  
84 ctatctgggg atcggttagg ttgcttcaat ctttcaatca aagggtcatgc tgagtgcgtc 1020  
86 aaattttatga gatcgttcaa tgttccccta ctgctcttgg gtggtggtgg ttacactatc 1080  
88 cgcaatgttg ccggttgcgt gtgctacgag actggagttg cacttgaggt tgaagttgaa 1140  
90 gacaagatgc cggagcatga atattatgaa tactttgggt cagactatac acttcacgtt 1200  
92 gctccaagta acatggaaaa taagaattct cgtcagatgc ttgaagagat tgcgaatgac 1260  
94 cttctccaca atctctctaa gcttcagcat gctccaagtg taccatttca ggaaagacca 1320  
96 cctgatacag agactcccga ggttgatgaa gaccaagaag atggggataa aagatgggat 1380  
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102 aaaggttgtg aggtggaggt ggatgagagt ggaagcacta aggttacagg agtaaaccca 1560  
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108 tgtctatcaa atgttgctag ttaagtttct ggagttgttg ttgttgtaag cactcctctg 1740  
110 ttttagagga ttgagcacgg atatgtattt attcgttgca tgtctgaatg atgatgatg 1800

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1807

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118 <211> LENGTH: 501
120 <212> TYPE: PRT
122 <213> ORGANISM: Arabidopsis thaliana
126 <400> SEQUENCE: 2
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134 Arg Lys Val Cys Tyr Phe Tyr Asp Pro Glu Val Gly Asn Tyr Tyr Tyr
136           20           25           30
140 Gly Gln Gly His Pro Met Lys Pro His Arg Ile Arg Met Thr His Ala
142           35           40           45
146 Leu Leu Ala His Tyr Gly Leu Leu Gln His Met Gln Val Leu Lys Pro
148           50           55           60
152 Phe Pro Ala Arg Glu Arg Asp Leu Cys Arg Phe His Ala Asp Asp Tyr
154   65           70           75           80
158 Val Ser Phe Leu Arg Ser Ile Thr Pro Glu Thr Gln Gln Asp Gln Ile
160           85           90           95
164 Arg Gln Leu Lys Arg Phe Asn Val Gly Glu Asp Cys Pro Val Phe Asp
166           100          105          110
170 Gly Leu Tyr Ser Phe Cys Gln Thr Tyr Ala Gly Gly Ser Val Gly Gly
172           115          120          125
176 Ser Val Lys Leu Asn His Gly Leu Cys Asp Ile Ala Ile Asn Trp Ala
178           130          135          140
182 Gly Gly Leu His His Ala Lys Lys Cys Glu Ala Ser Gly Phe Cys Tyr
184 145           150          155          160
188 Val Asn Asp Ile Val Leu Ala Ile Leu Glu Leu Leu Lys Gln His Glu
190           165          170          175
194 Arg Val Leu Tyr Val Asp Ile Asp Ile His His Gly Asp Gly Val Glu
196           180          185          190
200 Glu Ala Phe Tyr Ala Thr Asp Arg Val Met Thr Val Ser Phe His Lys
202           195          200          205
206 Phe Gly Asp Tyr Phe Pro Gly Thr Gly His Ile Gln Asp Ile Gly Tyr
208           210          215          220
212 Gly Ser Gly Lys Tyr Tyr Ser Leu Asn Val Pro Leu Asp Asp Gly Ile
214 225           230          235          240
218 Asp Asp Glu Ser Tyr His Leu Leu Phe Lys Pro Ile Met Gly Lys Val
220           245          250          255
224 Met Glu Ile Phe Arg Pro Gly Ala Val Val Leu Gln Cys Gly Ala Asp
226           260          265          270
230 Ser Leu Ser Gly Asp Arg Leu Gly Cys Phe Asn Leu Ser Ile Lys Gly
232           275          280          285
236 His Ala Glu Cys Val Lys Phe Met Arg Ser Phe Asn Val Pro Leu Leu
238           290          295          300
242 Leu Leu Gly Gly Gly Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp
244 305           310          315          320
248 Cys Tyr Glu Thr Gly Val Ala Leu Gly Val Glu Val Glu Asp Lys Met
250           325          330          335
254 Pro Glu His Glu Tyr Tyr Glu Tyr Phe Gly Pro Asp Tyr Thr Leu His

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260 Val Ala Pro Ser Asn Met Glu Asn Lys Asn Ser Arg Gln Met Leu Glu
262          355          360          365
266 Glu Ile Arg Asn Asp Leu Leu His Asn Leu Ser Lys Leu Gln His Ala
268          370          375          380
272 Pro Ser Val Pro Phe Gln Glu Arg Pro Pro Asp Thr Glu Thr Pro Glu
274 385          390          395          400
278 Val Asp Glu Asp Gln Glu Asp Gly Asp Lys Arg Trp Asp Pro Asp Ser
280          405          410          415
284 Asp Met Asp Val Asp Asp Asp Arg Lys Pro Ile Pro Ser Arg Val Lys
286          420          425          430
290 Arg Glu Ala Val Glu Pro Asp Thr Lys Asp Lys Asp Gly Leu Lys Gly
292          435          440          445
296 Ile Met Glu Arg Gly Lys Gly Cys Glu Val Glu Val Asp Glu Ser Gly
298          450          455          460
302 Ser Thr Lys Val Thr Gly Val Asn Pro Val Gly Val Glu Glu Ala Ser
304 465          470          475          480
308 Val Lys Met Glu Glu Gly Thr Asn Lys Gly Gly Ala Glu Gln Ala
310          485          490          495
314 Phe Pro Pro Lys Thr
316          500
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324 <211> LENGTH: 1800
326 <212> TYPE: DNA
328 <213> ORGANISM: Arabidopsis thaliana
332 <220> FEATURE:
334 <221> NAME/KEY: misc_feature
336 <222> LOCATION: (1374)
338 <223> OTHER INFORMATION: a or g or c or t/u
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344 gtgcccacaa ctctagtaa tgactttctc aggcattggt gacacaaatt ttgctctgag 60
346 taaaacttgg gaatagagag agactctgag tgagagagag attctgagtg agagacggag 120
348 atggaggcag acgaaagcgg catctctctg ccgtcgggac ccgacggagc taagcggcga 180
350 gtcagttact tctacgagcc gacgatcgga gactactact acggtcaagg ccaccgatg 240
352 aagcctcacc ggatccgtat ggctcatagc ctaatcattc actatcacct ccaccgtcgc 300
354 ttagaaatca gtgcacctag cctcgtctgac gcctccgata tcggccgatt ccattcgcgc 360
356 gagtatgttg acttcctcgc ttccgtttcg ccggaatcta tgggcgatec ttccgctgca 420
358 cgaaacctaa ggcgattcaa tgtcgttgag gattgtcctg tcttcgacgg actttttgat 480
360 ttttgccgtg cttccgcggg aggttctatt ggtgctgcgc tcaaattaaa cagacaggac 540
362 gctgatatcg ctatcaattg gggcgggtgg cttcaccatg ctaagaaaag cgaggcttct 600
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366 cgggttctct acatagatat tgatgtccac catggagatg gagtgaaga agcgttttac 720
368 accactgata gagttatgac tgtttctttc cacaaatttg gggacttttt ccaggaact 780
370 ggtcacataa gagatgttg cgtgaaaaa gggaaatact atgctctaaa tgttccacta 840
372 aacgatggta tggacgatga aagtttccgc agcttgttta gacctcttat ccagaagggt 900
374 atggaagtgt atcagccaga ggcagttggt cttcagtggt gtgctgactc cttaaagtgt 960
376 gatcggttgg gttgcttcaa cttatcagtc aagggtcacg ctgattgcct tcggttctta 1020
378 agactcttaca acgttctct catggtgttg ggtggtgaag ggtatactat tcgaaatggt 1080
380 gcccgttgct ggtgttatga gactgcagtt gctgttggag tagagccgga caacaaactc 1140

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382 ccttacaatg agtattttga gtatttcggc ccagattata cgtttcatgt cgacccaagt 1200
384 cctatggaga atttaaacac gcccaaagat atggagagga taaggaacac gttgctggaa 1260
386 caactttcgg gactaataca cgcacctagc gtccaqtttc agcacacacc accagtcaat 1320
W--> 388 cgagttttgg acgagccgga agatgacatg gagacaagac caaaacctcg catntggagt 1380
390 ggaactgcga cttatgaatc agacagtgc gatgatgata aacctcttca tggttactca 1440
392 tgtcgtggtg gcgcaactac ggacagggac tctaccggtg aagatgaaat ggatgacgat 1500
394 aacccagagc cagacgtgaa tctccatcg tcttaaacca gcttgatggt ttggtgtctc 1560
396 ttttgccata tgataatgtc ggcagattta agaaacaagt taggggaatg aatgattctt 1620
398 tgatgttttt tcagcaacct tttagattct gtgaaaacgc tgcattgatt agaacagtga 1680
400 caactgacta gtattttggc ccaagttaga aaatcagaat atgtgaaaaa aaaaaaaaaa 1740
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408 <211> LENGTH: 471
410 <212> TYPE: PRT
412 <213> ORGANISM: Arabidopsis thaliana
416 <220> FEATURE:
418 <221> NAME/KEY: UNSURE
420 <222> LOCATION: (418)
422 <223> OTHER INFORMATION: unknown or other
426 <400> SEQUENCE: 4
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434 Arg Lys Arg Arg Val Ser Tyr Phe Tyr Glu Pro Thr Ile Gly Asp Tyr
436           20           25           30
440 Tyr Tyr Gly Gln Gly His Pro Met Lys Pro His Arg Ile Arg Met Ala
442           35           40           45
446 His Ser Leu Ile Ile His Tyr His Leu His Arg Arg Leu Glu Ile Ser
448           50           55           60
452 Arg Pro Ser Leu Ala Asp Ala Ser Asp Ile Gly Arg Phe His Ser Pro
454   65           70           75           80
458 Glu Tyr Val Asp Phe Leu Ala Ser Val Ser Pro Glu Ser Met Gly Asp
460           85           90           95
464 Pro Ser Ala Ala Arg Asn Leu Arg Arg Phe Asn Val Gly Glu Asp Cys
466           100          105          110
470 Pro Val Phe Asp Gly Leu Phe Asp Phe Cys Arg Ala Ser Ala Gly Gly
472           115          120          125
476 Ser Ile Gly Ala Ala Val Lys Leu Asn Arg Gln Asp Ala Asp Ile Ala
478           130          135          140
482 Ile Asn Trp Gly Gly Gly Leu His His Ala Lys Lys Ser Glu Ala Ser
484   145          150          155          160
488 Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Gly Ile Leu Glu Leu Leu
490           165          170          175
494 Lys Met Phe Lys Arg Val Leu Tyr Ile Asp Ile Asp Val His His Gly
496           180          185          190
500 Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg Val Met Thr Val
502           195          200          205
506 Ser Phe His Lys Phe Gly Asp Phe Phe Pro Gly Thr Gly His Ile Arg
508           210          215          220
512 Asp Val Gly Ala Glu Lys Gly Lys Tyr Tyr Ala Leu Asn Val Pro Leu

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514 225                230                235                240
518 Asn Asp Gly Met Asp Glu Ser Phe Arg Ser Leu Phe Arg Pro Leu
520                245                250                255
524 Ile Gln Lys Val Met Glu Val Tyr Gln Pro Glu Ala Val Val Leu Gln
526                260                265                270
530 Cys Gly Ala Asp Ser Leu Ser Gly Asp Arg Leu Gly Cys Phe Asn Leu
532                275                280                285
536 Ser Val Lys Gly His Ala Asp Cys Leu Arg Phe Leu Arg Ser Tyr Asn
538                290                295                300
542 Val Pro Leu Met Val Leu Gly Gly Glu Gly Tyr Thr Ile Arg Asn Val
544 305                310                315                320
548 Ala Arg Cys Trp Cys Tyr Glu Thr Ala Val Ala Val Gly Val Glu Pro
550                325                330                335
554 Asp Asn Lys Leu Pro Tyr Asn Glu Tyr Phe Glu Tyr Phe Gly Pro Asp
556                340                345                350
560 Tyr Thr Leu His Val Asp Pro Ser Pro Met Glu Asn Leu Asn Thr Pro
562                355                360                365
566 Lys Asp Met Glu Arg Ile Arg Asn Thr Leu Leu Glu Gln Leu Ser Gly
568                370                375                380
572 Leu Ile His Ala Pro Ser Val Gln Phe Gln His Thr Pro Pro Val Asn
574 385                390                395                400
578 Arg Val Leu Asp Glu Pro Glu Asp Asp Met Glu Thr Arg Pro Lys Pro
580                405                410                415
W--> 584 Arg Xaa Trp Ser Gly Thr Ala Thr Tyr Glu Ser Asp Ser Asp Asp Asp
586                420                425                430
590 Asp Lys Pro Leu His Gly Tyr Ser Cys Arg Gly Gly Ala Thr Thr Asp
592                435                440                445
596 Arg Asp Ser Thr Gly Glu Asp Glu Met Asp Asp Asp Asn Pro Glu Pro
598                450                455                460
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604 465                470
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612 <211> LENGTH: 939
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626 cacgtttctc aggcateget tggagaatgt aaaaacaaga agggagagtt tgtgccttta 180
628 catgtaaagg ttgggaacca gaacttggtt ctgggaactc tatcgactga gaacatccct 240
630 cagctttttct gtgatttggt attcgacaag gagtttgagc tttctcacac ttggggaaaa 300
632 ggaagtgttt actttgttgg atacaaaact cccaacattg agccacaagg ctattctgag 360
634 gaagaagagg aagaagagga agaagttcct gctgggaatg ctgccaaagg tgtagctaaa 420
636 ccaaaggcta agcctgcaga agtgaagcca gctgttgatg atgaagagga tgagtctgat 480
638 tctgacggaa tggatgaaga tgattctgat ggtgaggatt ctgaggaaga agagcctaca 540
640 cctaagaagc ctgcatcaag caagaagaga gctaattgaa ctacccttaa agcacctgtg 600
642 tcagcaaaga aggcgaaagt agcagttact cctcagaaaa cagatgagaa gaagaaaggg 660
644 ggaaaggctg caaaccagag cccaaagtct gccagtcaag tctcatgtgg ttcattgca 720
646 aagactttca actcagggaa tgcatttgag tctcacaaca aggccaagca cgctgctgcc 780

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VERIFICATION SUMMARY

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Input Set : A:\104701.01 Sequence Listing.txt

Output Set: N:\CRF3\01112002\I645337.raw

L:388 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

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